



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 131977**

**TO: James Schultz**  
**Location: rem/2d18/2c18**  
**Art Unit: 1635**  
**Friday, September 17, 2004**  
**Case Serial Number: 10/019595**

**From: Paul Schulwitz**  
**Location: Biotech-Chem Library**  
**REM-1A65**  
**Phone: (571)272-2527**

**paul.schulwitz@uspto.gov**

### **Search Notes**

Examiner Schultz,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz  
Technical Information Specialist  
STIC Biotech/Chem Library  
(571)272-2527

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STIC-Biotech/ChemLib

131977

mq

From: Schultz, James  
Sent: Wednesday, September 08, 2004 1:49 PM  
To: STIC-Biotech/ChemLib  
Subject: Seq Search 10/019,595

Hello,  
Could you please run a length limited nucleotide sequence search on SEQ ID NO: 1 in the above entitled case which returns hits 30 nucleotides long and under?

Thanks,  
Doug Schultz

James Douglas Schultz, PhD  
AU 1635 (Biotechnology)  
Patent Examiner  
United States Patent and Trademark Office  
(Office) REM 2D18  
(Mail) REM 2C18  
(571) 272-0763

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SEP - 9 2004  
STIC

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2-\_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date Completed: 9/17  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

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Type of Search

NA Sequence: # \_\_\_\_\_  
AA Sequence :# \_\_\_\_\_  
Structure: # \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model  
Run on: September 15, 2004, 14:56:58 ; Search time 19497 Seconds  
(without alignments)  
11639.951 Million cell updates/sec  
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Perfect score: 5236  
Sequence: 1 cgagcggcgcccttgagc.....gtaccggatcctgaattc 5236

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
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Total number of hits satisfying chosen parameters: 1237800  
Minimum DB seq length: 0  
Maximum DB seq length: 30  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_hcg.\*  
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41: em\_htgo\_other.\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	24.4	0.5	29	6	AR162080	Sequence
2	24.4	0.5	29	6	AR166605	Sequence
3	24.4	0.5	29	6	BD238387	BD238387 Sorting o
4	24.4	0.5	29	6	AR279813	Sequence
5	24.4	0.5	29	6	AR288232	Sequence
6	24.4	0.5	29	6	AX048408	Sequence
7	24.4	0.5	29	6	AX048409	Sequence
8	24.4	0.5	29	6	AX052294	Sequence
9	24.4	0.5	29	6	AX353685	Sequence
10	24.4	0.5	29	6	AX662302	Sequence
11	24.4	0.5	29	6	BD204968	BD204968 Protein a
12	24.2	0.5	30	6	AR051244	Sequence
13	24.2	0.5	30	6	AR127791	Sequence
14	24.2	0.5	30	6	I28373	Sequence 12
15	24.2	0.5	24	6	AR009472	Sequence
16	24	0.5	24	6	E12007	Linker.. 9/1
17	23.8	0.5	28	6	BD234335	Improved
18	23.8	0.5	29	6	AX430216	Sequence
19	23.8	0.5	29	6	BD165919	BD165919 Method fo
20	23.4	0.4	26	6	I79496	Sequence 3
21	23.4	0.4	26	6	BD192375	Reagents
22	23.4	0.4	29	6	AX052989	Sequence
23	23	0.4	25	6	BD234336	Improved
24	22.8	0.4	26	6	AR174581	Sequence
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28	22.8	0.4	26	6	AR374073	Sequence
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43	22.4	0.4	24	6	AR105984	Sequence
44	22.4	0.4	24	6	AR107972	Sequence
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ALIGNMENTS

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LOCUS AR162080 29 bp DNA linear PAT 17-OCT-2001  
DEFINITION Sequence 8 from patent US 6258558.  
ACCESSION AR162080  
VERSION AR162080.1 GI:16229144  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Srostat,J.W., Roberts,R.W. and Liu,R.  
TITLE Method for selection of proteins using RNA-protein fusions  
JOURNAL Patent: US 6258558-A 9 10-JUL-2001;  
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RESULT 2
AR166605 LOCUS 29 bp DNA linear PAT 17-OCT-2001
DEFINITION Sequence 8 from patent US 6281344.
ACCESSION AR166605
VERSION AR166605.1 GI:16241997
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Szostak,J.W., Roberts,R.W. and Liu,R.
TITLE Nucleic acid-protein fusion molecules and libraries
JOURNAL Patent: US 6281344-A 8 28-AUG-2001;
FEATURES Location/Qualifiers
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RESULT 3
BD238387 LOCUS 29 bp DNA linear PAT 17-JUL-2003
DEFINITION Sorting of proteins using RNA-protein fused body.
ACCESSION BD238387
VERSION BD238387.1 GI:33048157
KEYWORDS JP 2002536025-A/5.
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1 (bases 1 to 29)
AUTHORS Szostak,J.W., Roberts,R.W. and Liu,R.
TITLE Sorting of proteins using RNA-protein fused body
JOURNAL Patent: JP 2002536025-A 5 29-OCT-2002;
COMMENT THE GENERAL HOSPITAL CORP
OS Artificial Sequence
PN JP 2002536025-A/5
PD 29-OCT-2002
PF 01-FEB-2000 JP 2000598669
PR 09-FEB-1999 US 09/247190
PI JACK W SZOSTAK, RICHARD W ROBERTS, RIHE LIU
PC C12N15/09, C07K1/00, C07K14/00, C12Q1/68, C12N15/00 CC
Translation template
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AR279813 LOCUS 29 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 8 from patent US 6518018.
ACCESSION AR279813
VERSION AR279813.1 GI:29714958
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Szostak,J.W. and Roberts,R.W.
TITLE RNA-antibody fusions and their selection
JOURNAL Patent: US 6518018-A 8 11-FEB-2003;
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DEFINITION Sequence 3 from patent US 6537749.
ACCESSION AR288232
VERSION AR288232.1 GI:31675516
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 29)
AUTHORS Kuimelis,R.G. and Wagner,R.
TITLE Addressable protein arrays
JOURNAL Patent: US 6537749-A 3 25-MAR-2003;
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AX048408/c LOCUS 29 bp DNA linear PAT 12-JAN-2001

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DEFINITION Sequence 7 from Patent WO0071747.
ACCESSION AX048408
VERSION AX048408.1 GI:12225572
KEYWORDS
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  artificial sequences.
ORGANISM
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REFERENCE
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AUTHORS Boekenkamp, D., Hoppe, H.U. and BURGSTALLER, P.
TITLE Detection system for separating constituents of a sample and
  production and use of the same
JOURNAL Patent: WO 0071747-A 7 30-NOV-2000;
  Aventis Research & Technologies GmbH & Co. KG (DE)
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RESULT 7
LOCUS AX048409 29 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 8 from Patent WO0071747.
ACCESSION AX048409
VERSION AX048409.1 GI:12225573
KEYWORDS
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ORGANISM
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REFERENCE
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AUTHORS Boekenkamp, D., Hoppe, H.U. and BURGSTALLER, P.
TITLE Detection system for separating constituents of a sample and
  production and use of the same
JOURNAL Patent: WO 0071747-A 8 30-NOV-2000;
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LOCUS AX052994 29 bp DNA linear PAT 12-JAN-2001
DEFINITION Sequence 10 from Patent WO0071749.
ACCESSION AX052994
VERSION AX052994.1 GI:12227096
KEYWORDS
  synthetic construct
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  artificial sequences.
ORGANISM
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REFERENCE
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AUTHORS Forster, A.C. and Blacklow, S.C.
TITLE Process and compositions for peptide, protein and peptidomimetic
  synthesis
JOURNAL Patent: WO 02059293-A 41 01-AUG-2002;
  Forster, Anthony C. (US); Blacklow, Stephen C. (US)

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REFERENCE
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AUTHORS Boekenkamp, D., Hoppe, H.U., BURGSTALLER, P., Konz, D., Woelk, U. and
  Pignot, M.
TITLE Detection system for analyzing molecular interactions, production
  and utilization thereof
JOURNAL Patent: WO 0071749-A 10 30-NOV-2000;
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LOCUS AX353685 29 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 5 from Patent WO0204656.
ACCESSION AX353685
VERSION AX353685.1 GI:18618749
KEYWORDS
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  artificial sequences.
ORGANISM
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REFERENCE
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AUTHORS Wagner, P. and Polakowski, T.
TITLE Bio-probes and use thereof
JOURNAL Patent: WO 0204656-A 5 17-JAN-2002;
  Xzillion GmbH & Co. KG (DE)
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LOCUS AX662302 29 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 41 from Patent WO02059293.
ACCESSION AX662302
VERSION AX662302.1 GI:29163186
KEYWORDS
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REFERENCE
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AUTHORS Forster, A.C. and Blacklow, S.C.
TITLE Process and compositions for peptide, protein and peptidomimetic
  synthesis
JOURNAL Patent: WO 02059293-A 41 01-AUG-2002;
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  ACCESSION
    BD204968
  VERSION
    BD204968.1 GI:33014738
  KEYWORDS
    JP 2002510505-A/3.
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  REFERENCE
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  AUTHORS
    Kuimelis,R.G. and Wagner,R.
  TITLE
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  JOURNAL
    Patent: JP 2002510505-A 3 09-APR-2002;
    PHYLLOS INC
  COMMENT
    OS Artificial Sequence
    PN JP 2002510505-A/3
    PD 09-APR-2002
    PF 31-MAR-1999 JP 2000542484
    PR 03-APR-1998 US 60/080686
    PT ROBERT G KUIMEELIS,RICHARD WAGNER
    PC C12N15/09,C07H21/02,C07H21/04,C12M1/00,C12Q1/68,G01N33/566, PC
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  AUTHORS
    Gryaznov,S.M.
  TITLE
    Convergent synthesis of branched and multiply connected
    macromolecular structures
  JOURNAL
    Patent: US 5830658-A 12 05-NOV-1996;
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  REFERENCE
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  AUTHORS
    Horn,T
  TITLE
    Synthesis of branched nucleic acids
  JOURNAL
    Patent: US 6180777-A 12 30-JAN-2001;
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  AUTHORS
    Gryaznov,S.M.
  TITLE
    Convergent synthesis of branched and multiply connected
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  JOURNAL
    Patent: US 5571677-A 12 05-NOV-1996;
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Db 1 CACACAAAAA 29

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TITLE
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JOURNAL
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Db 1 CACACAAAAA 29

RESULT 13
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    1 (bases 1 to 30)
  AUTHORS
    Horn,T
  TITLE
    Synthesis of branched nucleic acids
  JOURNAL
    Patent: US 6180777-A 12 30-JAN-2001;
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  REFERENCE
    1 (bases 1 to 30)
  AUTHORS
    Gryaznov,S.M.
  TITLE
    Convergent synthesis of branched and multiply connected
    macromolecular structures
  JOURNAL
    Patent: US 5571677-A 12 05-NOV-1996;
  FEATURES
    Location/Qualifiers
      1..30
        /organism="unknown"
        /mol_type="unassigned DNA"
ORIGIN
  Query Match
    0.5%; Score 24.2; DB 6; Length 30;
  Best Local Similarity
    89.7%; Pred. No. 2.4e+06;
  Matches
    26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5183 CTCCTCAACAAAAA 5211

```





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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.  
OM nucleic - nucleic search, using sw model  
Run on: September 15, 2004, 13:12:42 ; Search time 1798 Seconds  
(without alignments)  
12371.282 Million cell updates/sec  
Title: US-10-019-595-1  
Perfect score: 5236  
Sequence: 1 cgagcgcgccgcttgagc.....gtaccggatctctgaattc 5236  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 3373863 seqs, 2124099041 residues  
Total number of hits satisfying chosen parameters: 2723956  
Minimum DB seq length: 0  
Maximum DB seq length: 30  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : N\_Geneseq\_29Jan04:\*

1: Geneseqn1980s:.\*  
2: Geneseqn1980s:.\*  
3: Geneseqn2000s:.\*  
4: Geneseqn2001as:.\*  
5: Geneseqn2001bs:.\*  
6: Geneseqn2002s:.\*  
7: Geneseqn2003as:.\*  
8: Geneseqn2003bs:.\*  
9: Geneseqn2003cs:.\*  
10: Geneseqn2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24.4	0.5	29	3	AAA94315 RNA-prote
2	24.4	0.5	29	4	AAS0066 Synthetic
3	24.4	0.5	29	4	AAS0066 Synthetic
4	24.4	0.5	29	4	AAS0066 Synthetic
5	24.4	0.5	29	6	AAS0066 Synthetic
6	24.2	0.5	30	2	AAV48087 Oligonuc
7	24.2	0.5	30	2	AAQ83940 Oligonuc
8	24.2	0.5	30	2	AAQ83940 Oligonuc
9	23.8	0.5	28	3	AAA40358 pBluescri
10	23.8	0.5	28	3	AAA40358 pBluescri
11	23.4	0.4	25	2	AAV48087 Oligonuc
12	23.4	0.4	25	2	AAV48087 Oligonuc
13	23.4	0.4	26	2	AAV71936 Anchored
14	23.4	0.4	27	2	AAV71936 Anchored
15	23.2	0.4	29	4	AAV71936 Anchored
16	23.2	0.4	29	4	AAV71936 Anchored
17	23.2	0.4	29	4	AAV71936 Anchored
18	23.2	0.4	29	4	AAV71936 Anchored
19	23.2	0.4	29	4	AAV71936 Anchored
20	23.2	0.4	30	4	AAV71936 Anchored
21	22.8	0.4	26	4	AAV71936 Anchored
22	22.8	0.4	26	6	AAV71936 Anchored
23	22.8	0.4	26	6	AAV71936 Anchored

ALIGNMENTS

RESULT 1  
AAA94315  
ID AAA94315 standard; DNA; 29 BP.  
XX  
AC AAA94315;  
XX  
DT 11-JAN-2001 (first entry)  
XX  
DE RNA-protein fusion oligonucleotide 30-P.  
XX  
KW RNA-protein fusion; protein library; protein isolation; gene cloning; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 29  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "attached to puromycin, a peptide acceptor"  
XX  
PN WO200047775-A1.  
XX  
PD 17-AUG-2000.  
XX  
PF 01-FEB-2000; 2000WO-US002589.  
XX  
PR 09-FEB-1999; 99US-00247190.  
XX  
PA (GEO ) GEN HOSPITAL CORP.  
XX  
PI Szostak JW, Roberts RW, Liu R;  
XX  
PS WPI; 2000-533022/48.  
XX  
PT Producing protein or DNA libraries which are useful for improving  
PT existing proteins, by in vitro translating protein coding sequences to  
PT produce RNA-protein fusions and incubating these protein fusions under  
PT high salt conditions.  
XX  
PS Disclosure; Page 43; 121pp; English.  
XX  
CC The present sequence is one of a number of oligonucleotides which were  
CC used for the generation of RNA-protein fusions, including fusions having  
CC a myc epitope tag. The RNA-protein fusions comprise a protein covalently  
CC linked to the 3' end of its own mRNA. This is accomplished by synthesis  
CC and in vitro or in situ translation of an mRNA molecule with a peptide

ALIGNMENTS

RESULT 1  
AAA94315  
ID AAA94315 standard; DNA; 29 BP.  
XX  
AC AAA94315;  
XX  
DT 11-JAN-2001 (first entry)  
XX  
DE RNA-protein fusion oligonucleotide 30-P.  
XX  
KW RNA-protein fusion; protein library; protein isolation; gene cloning; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 29  
FT /\*tag= a  
FT /mod\_base= OTHER  
FT /note= "attached to puromycin, a peptide acceptor"  
XX  
PN WO200047775-A1.  
XX  
PD 17-AUG-2000.  
XX  
PF 01-FEB-2000; 2000WO-US002589.  
XX  
PR 09-FEB-1999; 99US-00247190.  
XX  
PA (GEO ) GEN HOSPITAL CORP.  
XX  
PI Szostak JW, Roberts RW, Liu R;  
XX  
PS WPI; 2000-533022/48.  
XX  
PT Producing protein or DNA libraries which are useful for improving  
PT existing proteins, by in vitro translating protein coding sequences to  
PT produce RNA-protein fusions and incubating these protein fusions under  
PT high salt conditions.  
XX  
PS Disclosure; Page 43; 121pp; English.  
XX  
CC The present sequence is one of a number of oligonucleotides which were  
CC used for the generation of RNA-protein fusions, including fusions having  
CC a myc epitope tag. The RNA-protein fusions comprise a protein covalently  
CC linked to the 3' end of its own mRNA. This is accomplished by synthesis  
CC and in vitro or in situ translation of an mRNA molecule with a peptide

CC acceptor attached to its 3' end. The RNA-protein fusions are incubated  
 CC under high salt conditions to produce a protein library. This method is  
 CC useful for improving or altering existing proteins, as well as for  
 CC isolating new proteins and nucleic acid or small molecule targets. It may  
 CC also be used to improve human or humanised single-chain antibodies for  
 CC the treatment of a number of diseases. The method is useful for the  
 CC isolation of proteins with specific binding properties, for screening  
 CC cDNA libraries and cloning new genes on the basis of protein-protein  
 CC interactions. Unlike prior art, the new method does not rely on  
 CC maintaining the integrity of an mRNA:ribosome:nascent chain ternary  
 CC complex, which is very fragile and is therefore of limited use. The  
 CC method does not rely on topological links between the protein and the  
 CC nucleic acid so that the information of the protein is retained and can  
 CC be recovered in readable, nucleic acid form

XX Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;  
 CC Query Match 0.5%; Score 24.4; DB 3; Length 29;  
 CC Best Local Similarity 96.2%; Pred. No. 8.6e+04;  
 CC Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5188 AACAAAAA...AAAAAACC 5213  
 DB 4 AAAAAA...AAAAAACC 29

## RESULT 2

AAS00066  
 ID AAS00066 standard; DNA; 29 BP.

XX AAS00066;

DT 12-SEP-2001 (first entry)

DE Synthetic branched encoding molecule sequence.

XX Addressing element; microarray; protein display;

KW Branched encoding molecule; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT modified\_base 9..10

FT /\*tag= a

FT /mcd\_base= OTHER

FT /note= "AXA, where X is a branching monomer, linked to  
 FT nucleotide 16 of sequence in AAS00065 via a (Hexaethylene  
 FT oxide)n linkage"

FT modified\_base 30

FT /\*tag= b

FT /mcd\_base= OTHER

FT /note= "Other= Covalently linked to puromycin"

XX WO200116352-A1.

XX 08-MAR-2001.

XX 25-AUG-2000; 2000WO-US023414.

XX 27-AUG-1999; 99US-0151261P.

XX (PHYL-) PHYLLOS INC.

XX Kuimelis RG;

XX WPI; 2001-183261/18.

XX Encoding and sorting in vitro translated proteins, useful for the  
 PT identification of desired binding partners, comprises attaching a nucleic  
 PT acid linker to the protein and binding an encoding molecule to the  
 PT linker.

PS Example 3; Fig 9B; 48pp; English

XX The sequence represents part of a branched encoding molecule used in  
 CC methods to hybridise a capture probe to the addressing element of a DNA  
 CC linker attached to an in vitro translated protein, in order to immobilise  
 CC the protein to a solid support. The new methods are useful for tagging or  
 CC encoding in vitro translated proteins with unique and minimal encoding  
 CC molecules and sorting these molecules onto solid supports. They are also  
 CC useful for the identification of a desired binding partner. The method  
 CC allows the use of pre-made sets of universal encoding molecules, such as  
 CC nucleic acid(s) (analogues). These can be used in conjunction with  
 CC corresponding universal microarrays or sets of microparticles to create  
 CC new protein display systems which are flexible, modular, scalable and  
 CC cost effective. The method allows the use of nucleic acid analogue which  
 CC are not susceptible to enzymatic incorporation or polymerisation and are  
 CC superior to conventional DNA/RNA. The proteins can also be labelled with  
 CC fluorescent groups which can be used to monitor the protein in real time.  
 CC The absence of RNA is advantageous as they can adopt secondary structures  
 CC which are difficult to predict and can interfere with hybridisation steps  
 CC and protein folding/function

XX Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

CC Query Match 0.5%; Score 24.4; DB 4; Length 29;

CC Best Local Similarity 96.2%; Pred. No. 8.6e+04;

CC Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5188 AACAAAAA...AAAAAACC 5213

DB 4 AAAAAA...AAAAAACC 29

## RESULT 3

AAS00990

ID AAS00990 standard; DNA; 29 BP.

XX AAS00990;

DT 31-AUG-2001 (first entry)

DE C-myc epitope puromycin linker primer #1.

XX C-myc; epitope; detection; amplification; biomedical diagnosis;  
 KW environmental monitoring; primer; ss.

XX Unidentified.

XX WO200142494-A2.

XX 14-JUN-2001.

XX 20-OCT-2000; 2000WO-EP010336.

XX 10-DEC-1999; 99DE-01059857.

XX (AVET) AVENTIS RES & TECHNOLOGIES GMBH & CO KG.

XX Burgstaller P, Konz D;

XX WPI; 2001-381706/40.

XX System for detecting immobilized analyte, useful e.g. for biomedical  
 PT diagnosis, has as detection agent specific polypeptide coupled to nucleic  
 PT acid for signal amplification.

XX Example; Page 6; 12pp; German.

XX This invention describes a novel test system (A) which comprises at least  
 CC one immobilized analyte (I) on an insoluble carrier and a polypeptide  
 CC detection agent (II), specific for (I) and conjugated, via a linker, to  
 CC an amplifier (III). (A) is used for direct, in vitro detection of (I)  
 CC with amplification of the signal by polymerase chain reaction (PCR), or a  
 CC related technique, applied to (III). The method is useful in biomedical  
 CC diagnosis and environmental monitoring and can be used for detecting

CC range of (1), e.g. diagnostic or pharmaceutical agents, secondary  
CC metabolites, herbicides or pesticides. (A) allow simultaneous, parallel  
CC detection of many different analytes (high throughput capacity),  
CC relatively simply (only a few incubation and washing steps are required)  
CC and with high sensitivity and selectivity. This sequence represents  
CC primer used in the amplification of the c-myc DNA fragment which encodes  
CC an epitope used to illustrate the method of the invention  
XX  
SQ Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;  
  
Query Match 0.5%; Score 24.4; DB 4; Length 29;  
Best Local Similarity 96.2%; Pred. No. 8.6e+04;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5188 AACAAAAA... 5213  
DB 4 AAAAAA... 29  
  
RESULT 4  
ID AAK98637 standard; DNA; 29 BP.  
AC AAK98637;  
XX  
DT 19-APR-2002 (first entry)  
XX  
DE S cerevisiae alpha factor receptor STE2 vector linker.  
XX  
KW Biological material detection; electrophoresis; bioprobe isolation;  
KW alpha factor receptor; STE2; linker; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 29 /\*tag= a  
FT /\*mod\_base= OTHER  
FT /\*note= "modified by puromycin"  
XX  
PN WO200204656-A2.  
XX  
PD 17-JAN-2002.  
XX  
PE 26-JUN-2001; 2001WO-EP007259.  
XX  
PR 07-JUL-2000; 2000DE-01033194.  
XX  
PA (XZIL-) XZILLION GMBH & CO KG.  
XX  
PI Wagner P, Polakowski T;  
XX  
DR WI; 2002-154934/20.  
XX  
PT Detecting and purifying biological material by (di)electrophoresis,  
PT useful e.g. for separating tissues and viruses, comprises using a probe  
PT that alters (di)electrophoretic properties.  
XX  
PS Example 1; Page 12; 20pp; German.  
XX  
CC The present invention relates to a method for the detection or  
CC purification of biological material by electrophoresis, which comprises  
CC (i) treating the biological material containing different species with a  
CC bioprobe and (ii) establishing an electric field for detection or  
CC purification of at least one complex formed between the biological  
CC material being tested and a specifically bound bioprobe. The method is  
CC used for detection and purification of tissue, cells, cell organelles,  
CC viruses, proteins, nucleic acids, lipids and/or other organic compounds.  
CC It can also be used for the isolation of specific bioprobes from a  
CC library of bioprobes. The present sequence is a linker described in the  
CC exemplification of the invention  
XX  
SQ Sequence 29 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.5%; Score 24.4; DB 6; Length 29;  
Best Local Similarity 96.2%; Pred. No. 8.6e+04;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5188 AACAAAAA... 5213  
DB 4 AAAAAA... 29  
  
RESULT 5  
ID AAV48087 standard; DNA; 30 BP.  
XX  
AC AAV48087;  
XX  
DT 27-OCT-1998 (first entry)  
XX  
DE Oligonucleotide 30-P.  
XX  
KW In situ translation; RNA-protein fusion; binding reagent; antibody;  
KW industrial catalyst; ss.  
XX  
OS Synthetic.  
XX  
FH Key Location/Qualifiers  
FT modified\_base 30 /\*tag= a  
FT /\*note= "Puromycin"  
XX  
PN WO9831700-A1.  
XX  
PD 23-JUL-1998.  
XX  
PE 14-JAN-1998; 98WO-US000807.  
XX  
PR 21-JAN-1997; 97US-0035963P.  
PR 06-NOV-1997; 97US-0064491P.  
XX  
PA (GEO) GEN HOSPITAL CORP.  
XX  
PI Szostak JW, Roberts RW, Liu R;  
XX  
DR WPI; 1998-414032/35.  
XX  
PT Selection of specific protein by screening protein-RNA fusions generated  
PT in vitro or in situ - useful for, e.g. identifying enzymes and antibodies  
PT with altered properties, potentially useful as catalysts or for therapy  
PT or diagnosis.  
XX  
PS Disclosure; Page 39; 94pp; English.  
XX  
CC The Oligonucleotides AAV48087, AAV48089-V48091 and AAV48096-V48098 and  
CC variations were used to generate RNA-protein fusions. These were used in  
CC the selection of a specific protein or RNA, by in vitro or in situ  
CC translation of candidate RNA molecules to produce RNA-protein fusions,  
CC then selecting specific RNA protein fusions. The method is used to select  
CC proteins (or DNA encoding them) having altered properties, e.g. for  
CC identification of new binding reagents, to identify improved human  
CC antibodies or new enzymes. These proteins are potentially useful in  
CC diagnosis and therapy, or as industrial catalysts. The methods allow many  
CC rounds of selection and amplification to be performed, resulting in  
CC enrichment of even very rare molecules and allowing isolation of proteins  
CC that bind specifically to almost any compound or catalyse almost any  
CC reaction  
XX  
SQ Sequence 30 BP; 27 A; 2 C; 0 G; 0 T; 0 U; 1 Other;  
  
Query Match 0.5%; Score 24.4; DB 2; Length 30;  
Best Local Similarity 96.2%; Pred. No. 8.8e+04;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 5188 AACAAAAA... 5213





CC Mononucleotide repeat locus BAT25, and was used to illustrate the  
 CC invention

XX Sequence 29 BP; 26 A; 2 C; 0 G; 1 T; 0 U; 0 Other;

Query Match 0.5%; Score 23.8; DB 6; Length 29;  
 Best Local Similarity 92.6%; Pred. No. 1.2e+05;  
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5188 AACACAAAAA...AACCA 5214

DB 3 AAAAAA...AATCA 29

RESULT-11

AAx84258/c

ID AAX84258 standard; DNA; 25 BP.

AC AAX84258;

XX 08-SEP-1999 (first entry)

DE PCR primer for human Nck associated protein 1 coding sequence.

XX Nck associated protein 1; Napi; human; apoptosis; Alzheimer's disease;  
 KW therapy; PCR primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9931239-A1.

XX 24-JUN-1999.

XX 14-DEC-1998; 98WO-JP005646.

XX 15-DEC-1997; 97JP-00363183.

XX (KYOW ) KYOWA HAKKO KOGYO KK.

PA (SAKA/) SAKAKI Y.

XX Sakaki Y;

PI WPI; 1999-395181/33.

XX Protein inhibiting apoptosis, useful in the diagnosis and treatment of  
 PT Alzheimer's disease.

XX Example 1; Page 76; 90pp; Japanese.

XX This sequence represents a PCR primer used to isolate DNA encoding the  
 CC human Nck associated protein 1 (Napi) of the invention. Napi inhibits  
 CC apoptosis. The protein can be used in the investigation, diagnosis and  
 CC treatment (e.g. by gene therapy) of Alzheimer's disease

XX Sequence 25 BP; 0 A; 0 C; 1 G; 24 T; 0 U; 0 Other;

Query Match 0.4%; Score 23.4; DB 2; Length 25;

Best Local Similarity 96.0%; Pred. No. 1.4e+05;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5187 CAACAAAAA...AAAAA 5211

DB 25 CAAAAA...AAAAA 1

RESULT 12

AAx07466/c

ID AAX07466 standard; cDNA; 26 BP.

XX AAX07466;

XX 08-JUN-1999 (first entry)

DT

XX Human BS124 specific EST clone oligonucleotide.

DE BS124; breast; cancer; detection; diagnosis; prevention; treatment; EST;  
 KW ss.

XX Synthetic.

OS WO9859049-A1.

XX 30-DEC-1998.

XX 19-JUN-1998; 98WO-US012862.

XX 20-JUN-1997; 97US-00879354.

XX (ABBO ) ABBOTT LAB.

XX Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;

PI Granados-EN, Hodges SC, Klaes MR, Kratochvil JD, Russell JC;

PI Scheffel CP, Stroupe SD, Yu H;

XX WPI; 1999-105623/09.

XX New isolated BS124 polynucleotides and polypeptides - used for detecting,  
 PT diagnosing, preventing or treating diseases or conditions of the breast,  
 PT such as breast cancer.

XX Disclosure; Page 97; 125pp; English.

XX The sequence is that of an oligonucleotide used in the isolation of a  
 CC BS124-specific EST clone. It is useful for detecting, diagnosing,  
 CC staging, preventing or treating, or determining predisposition to  
 CC diseases or conditions of the breast, such as breast cancer

XX Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;

Query Match 0.4%; Score 23.4; DB 2; Length 26;

Best Local Similarity 96.0%; Pred. No. 1.4e+05;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5187 CAACAAAAA...AAAAA 5211

DB 26 CAAAAA...AAAAA 2

RESULT 13

AAx78723/c

ID AAX78723 standard; DNA; 26 BP.

XX AAX78723;

XX 03-SEP-1999 (first entry)

XX Human pancreatic PA153 EST-specific clone primer 12.

XX Pancreatic disease; PA153; human; cytostatic; detection; antigen;  
 KW anti-PA153; antagonist; therapy; treatment; tumour; metastasis;  
 KW gene therapy; EST; expressed sequence tag; primer; ss.

XX Synthetic.

OS Homo sapiens.

XX WO9931274-A2.

XX 24-JUN-1999.

XX 11-DEC-1998; 98WO-US026441.

XX 15-DEC-1997; 97US-00990568.

XX (ABBO ) ABBOTT LAB.

XX



PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Roberts-Rapp L;  
PI Russell JC, Stroupe SD;  
XX WPI; 1999-405041/34.  
XX PA153 cDNA transcribed from pancreatic tissue.  
XX Example 2; Page 121; 123pp; English.  
XX This invention describes novel contiguous and partially overlapping cDNA  
sequences and their encoded polypeptides, designated PA153, transcribed  
from human pancreatic tissue and which have cytostatic activity. The  
cDNA sequences are all useful in methods  
of detection. Detection of PA153 polynucleotide, antigens or anti-PA153  
antibodies in a sample is indicative of pancreatic disease. PA153  
antibodies (antagonists) can also be used in vivo for therapeutic use,  
e.g. treatment of pancreatic disease, tumours or metastases. Antisense  
PA153 polynucleotides can be used in gene therapy of pancreatic diseases.  
XX RAX78712-X78725 represent primers used in the method of the invention  
XX SQ Sequence 26 BP; 0 A; 0 C; 1 G; 25 T; 0 U; 0 Other;  
Query Match 0.4%; Score 23.4; DB 2; Length 26;  
Best Local Similarity 96.0%; Pred. No. 1.4e+05;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5187 CAACAAAAA AAAAAAAAAA AAAAAA 5211  
DB 26 CAAAAA AAAAAAAAAA AAAAAA AAAAAA 2  
RESULT 14  
AAV71936/c  
ID AAV71936 standard; DNA; 27 BP.  
AC AAV71936;  
XX 18-FEB-1999 (first entry)  
XX Anchored poly T RT-PCR primer.  
XX Normalised; cDNA library; mRNA cloning; reverse transcription;  
XX immobilise; screening; hybridisation; nucleic acid amplification;  
XX expression pattern; drug development; PCR primer; RT-PCR; ss.  
XX Synthetic.  
XX WO9851789-A2.  
XX 19-NOV-1998.  
XX 13-MAY-1998; 98WO-DK000186.  
XX 13-MAY-1997; 97DK-0000547.  
XX 19-MAY-1997; 97US-00871030.  
XX 27-MAR-1998; 98DK-00000432.  
XX (DISP-) DISPLAY SYSTEMS BIOTECH APS.  
XX Warthoe PR;  
XX WPI; 1999-009772/01.  
XX Preparation of normalised, subdivided cDNA libraries from mRNA - by  
reverse transcription and amplification, used to screen for new genes and  
interacting proteins, potential drugs, and for diagnosis.  
XX Example 1; Page 29; 71pp; English.  
XX The invention relates to preparation of a normalised, subdivided library  
of amplified cDNA from the coding regions of mRNA in a sample. The method  
involves reverse transcription, with at least one cDNA primer of formula

CC 5'-Conl-dTn2-Vn3-Nn4 to form first stand cDNA where Con1 = any sequence  
of 1-100 nucleotides; dT = deoxythymidyl; n2 is at least 1; n3 and n4  
are both 0, or n3 is 1 and n4 is at least 1; followed by second strand  
cDNA synthesis using the first strand as template and a second cDNA  
primer of a similar formula, in the presence of DNA polymerase I (or its  
Klenow fragment) and amplification of double-stranded cDNA with a set of  
amplification primers. Comparison of cDNA in the prepared library with a  
database (a computer-generated list of molecular weights of restricted  
DNA fragments of known sequence) is used to determine presence of an  
expressed protein in a cell, also to detect changes in such expression  
(particularly for diagnosis of disease). Surfaces (chip) having amplified  
cDNA stably immobilised on it, obtained by a similar method, are used to  
screen for genes of a particular family, by hybridisation with nucleic  
acid from the family (to identify new genes) and to detect differences in  
expression patterns between cells. The polypeptides expressed by the  
libraries can be used for drug development. Sequences AAV71935 to  
AAV71946 represent primers used to exemplify the method of the invention  
XX SQ Sequence 27 BP; 0 A; 1 C; 1 G; 25 T; 0 U; 0 Other;  
Query Match 0.4%; Score 23.4; DB 2; Length 27;  
Best Local Similarity 96.0%; Pred. No. 1.4e+05;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 5187 CAACAAAAA AAAAAAAAAA AAAAAA 5211  
DB 26 CAAAAA AAAAAAAAAA AAAAAA AAAAAA 2  
RESULT 15  
AAV74918  
ID AAV74918 standard; DNA; 29 BP.  
XX AAV74918;  
XX 23-MAY-2001 (first entry)  
XX CD40L poly-A tract sequence SEQ ID NO:15.  
XX Human; CD40L; promoter; CD40 ligand promoter; rheumatoid arthritis;  
XX diagnosis; antiarthritic; antirheumatic; immunosuppressive;  
XX antinflammatory; inflammatory disease; autoimmune disease; ds.  
XX Homo sapiens.  
XX WO200119844-A1.  
XX 22-MAR-2001.  
XX 13-SEP-2000; 2000WO-US024966.  
XX 13-SEP-1999; 99US-0153625P.  
XX (NYRE-) NEW YORK SOC RELIEF RUPTURED & CRIPPLED.  
XX Crow MK, Li Y;  
XX WPI; 2001-244776/25.  
XX New altered CD40L promoter for use in the study, diagnosis and treatment  
of a variety of inflammatory disorders and autoimmune diseases, such as  
rheumatoid arthritis.  
XX Example 1; Fig 3; 90pp; English.  
XX The present invention describes an isolated, purified nucleic acid, which  
is an altered CD40 ligand (CD40L) promoter (I) for CD40 ligand, having  
residues 331-455 of the sequence comprising 455 nucleotides given in  
AAV4905 where A in the wild type sequence at position 331 (corresponding  
to position -125) is replaced with C. (I) has antiarthritic,  
CC antirheumatic, immunosuppressive and antiinflammatory activities, and can  
be used in gene therapy. (I) is useful in the study, diagnosis and  
treatment of inflammatory and autoimmune diseases, as well as diseases in

CC which elevated expression of CD40L is a factor, e.g., rheumatoid  
CC arthritis. The present sequence represents a CD40L poly-A tract sequence  
CC which is used in an example from the present invention

XX  
SQ Sequence 29 BP; 23 A; 3 C; 0 G; 3 T; 0 U; 0 Other;

Query Match 0.4%; Score 23.2; DB 4; Length 29;  
Best Local Similarity 89.3%; Pred. No. 1.6e+05;  
Matches 25; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5188 AACCAAAAAAAAAAAAAAAAAAACCAT 5215

Db 1 AAAAAAAAAAAAAAAAAACAAACCTT 28

Search completed: September 15, 2004, 16:54:03  
Job time : 1802 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 16:11:08 ; Search time 323 Seconds  
(without alignments)  
8996.046 Million cell updates/sec

Title: US-10-019-595-1  
Perfect score: 5236  
Sequence: 1 cgagcgcgccgttgcgc.....gtaccggatctctgaattc 5236

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 628400

Minimum DB seq length: 0  
Maximum DB seq length: 30

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*  
1: /cgn2\_6/prodata/2/ina/5A\_COMB.seq:\*  
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5: /cgn2\_6/prodata/2/ina/6C\_COMB.seq:\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24.4	0.5	29	3	US-09-244-794A-8
2	24.4	0.5	29	3	US-09-007-005-8
3	24.4	0.5	29	3	US-09-247-190-8
4	24.4	0.5	29	3	US-09-244-796-8
5	24.4	0.5	29	4	US-09-238-710-8
6	24.4	0.5	29	4	US-09-282-734-3
7	24.2	0.5	30	1	US-08-455-627-12
8	24.2	0.5	30	2	US-08-589-856-12
9	24.2	0.5	30	3	US-08-787-321-12
10	24	0.5	24	1	US-08-566-037A-22
11	23.8	0.5	29	4	US-10-003-998A-7
12	23.4	0.4	26	1	US-08-621-914A-3
13	23.4	0.4	30	1	US-09-648-040-4
14	22.8	0.4	26	1	US-08-621-914A-1
15	22.8	0.4	26	4	US-09-522-217-38
16	22.8	0.4	26	4	US-09-527-345-7
17	22.8	0.4	26	4	US-09-923-246-38
18	22.8	0.4	26	4	US-10-295-723-38
19	22.6	0.4	26	4	US-09-527-345-6
20	22.6	0.4	26	4	US-09-157-513-10
21	22.6	0.4	26	4	US-08-161-939A-43
22	22.6	0.4	29	4	US-08-227-476-5
23	22.4	0.4	24	1	US-08-014-943A-25
24	22.4	0.4	24	1	US-08-486-421-50
25	22.4	0.4	24	1	US-08-470-911-50
26	22.4	0.4	24	2	US-08-735-381-1
27	22.4	0.4	24	2	US-08-486-809-50

28 22.4 0.4 24 3 US-09-183-619-7 Sequence 7, Appli  
29 22.4 0.4 24 3 US-09-201-674-1 Sequence 1, Appli  
30 22.4 0.4 24 4 US-09-536-936-11 Sequence 11, Appli  
31 22.4 0.4 24 4 US-09-025-639-4 Sequence 4, Appli  
32 22.4 0.4 24 4 US-09-333-237-4 Sequence 4, Appli  
33 22.4 0.4 24 4 US-09-732-067-1 Sequence 1, Appli  
34 22.4 0.4 24 4 US-10-043-415-4 Sequence 4, Appli  
35 22.4 0.4 24 4 US-09-854-317-1 Sequence 1, Appli  
36 22.4 0.4 24 4 US-09-721-154-1 Sequence 1, Appli  
37 22.4 0.4 25 1 US-08-341-148-2 Sequence 2, Appli  
38 22.4 0.4 25 1 US-08-460-130-2 Sequence 2, Appli  
39 22.4 0.4 25 3 US-08-969-813-1 Sequence 1, Appli  
40 22.4 0.4 25 3 US-09-183-619-5 Sequence 5, Appli  
41 22.4 0.4 25 4 US-09-282-734-23 Sequence 23, Appli  
42 22.4 0.4 25 5 PCT-US94-14096-2 Sequence 2, Appli  
43 22.4 0.4 26 1 US-08-621-914A-3 Sequence 2, Appli  
44 22.4 0.4 26 3 US-08-873-437-2 Sequence 2, Appli  
45 22.4 0.4 26 3 US-09-197-951-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1  
US-09-244-794A-8  
; Sequence 8, Application US/09244794A  
; Patent No. 6214553  
; GENERAL INFORMATION:  
; APPLICANT: Szostak, Jack W.  
; APPLICANT: Roberts, Richard W.  
; APPLICANT: Liu, Rihe  
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN  
; FILE REFERENCE: 00786/350006  
; CURRENT APPLICATION NUMBER: US/09/244,794A  
; CURRENT FILING DATE: 1999-02-05  
; PRIOR APPLICATION NUMBER: 60/035,963  
; PRIOR FILING DATE: 1997-01-27  
; PRIOR APPLICATION NUMBER: 60/064,491  
; PRIOR FILING DATE: 1997-11-06  
; PRIOR APPLICATION NUMBER: 09/007,005  
; PRIOR FILING DATE: 1998-01-14  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Translation template  
US-09-244-794A-8

Query Match 0.5%; Score 24.4; DB 3; Length 29;  
Best Local Similarity 96.2%; Pred. No. 6e+03;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5188 AACAAAAA...AAAAAACCC 5213  
Db 4 AAAAAA...AAAAAACCC 29

RESULT 2  
US-09-007-005-8  
; Sequence 8, Application US/09007005B  
; Patent No. 6258558  
; GENERAL INFORMATION:  
; APPLICANT: Szostak, Jack W.  
; APPLICANT: Roberts, Richard W.  
; APPLICANT: Liu, Rihe  
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN  
; FILE REFERENCE: 00786/350003  
; CURRENT APPLICATION NUMBER: US/09/007,005B

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; CURRENT FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-007-005-8

Query Match      0.5%; Score 24.4; DB 3; Length 29;
Best Local Similarity 96.2%; Pred. No. 6e+03;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5188 AACAAAAA...AAAAAACC 5213
Db 4 AAAAAA...AAAAAACC 29

RESULT 3
US-09-247-190-8
; Sequence 8, Application US/09247190
; Patent No. 6261804
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350005
; CURRENT APPLICATION NUMBER: US/09/247,190
; EARLIER FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-21
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-247-190-8

Query Match      0.5%; Score 24.4; DB 3; Length 29;
Best Local Similarity 96.2%; Pred. No. 6e+03;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5188 AACAAAAA...AAAAAACC 5213
Db 4 AAAAAA...AAAAAACC 29

RESULT 4
US-09-244-796-8
; Sequence 8, Application US/09244796
; Patent No. 6261344
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350007

; CURRENT APPLICATION NUMBER: US/09/244,796
; CURRENT FILING DATE: 1999-02-05
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-244-796-8

Query Match      0.5%; Score 24.4; DB 3; Length 29;
Best Local Similarity 96.2%; Pred. No. 6e+03;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5188 AACAAAAA...AAAAAACC 5213
Db 4 AAAAAA...AAAAAACC 29

RESULT 5
US-09-238-710-8
; Sequence 8, Application US/09238710A
; Patent No. 6518018
; GENERAL INFORMATION:
; APPLICANT: Szostak, Jack W.
; APPLICANT: Roberts, Richard W.
; APPLICANT: Liu, Rihe
; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
; FILE REFERENCE: 00786/350004
; CURRENT APPLICATION NUMBER: US/09/238,710A
; EARLIER FILING DATE: 1999-01-28
; EARLIER APPLICATION NUMBER: 60/035,963
; EARLIER FILING DATE: 1997-01-27
; EARLIER APPLICATION NUMBER: 60/064,491
; EARLIER FILING DATE: 1997-11-06
; EARLIER APPLICATION NUMBER: 09/007,005
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
US-09-238-710-8

Query Match      0.5%; Score 24.4; DB 4; Length 29;
Best Local Similarity 96.2%; Pred. No. 6e+03;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5188 AACAAAAA...AAAAAACC 5213
Db 4 AAAAAA...AAAAAACC 29

RESULT 6
US-09-282-734-3
; Sequence 3, Application US/09282734A
; Patent No. 6537749
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kuimelis et al.
; TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS
; FILE REFERENCE: 50036/009002

```

[illegible]

```

RESULT 9
US-08-787-321-12
; Sequence 12, Application US/08787321A
; Patent No. 6180777
; GENERAL INFORMATION:
; APPLICANT: Horri, Thomas
; TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
; FILE REFERENCE: (1300)-1199.002
; CURRENT APPLICATION NUMBER: US/08/787.321A
; CURRENT FILING DATE: 1997-01-03
; EARLIER APPLICATION NUMBER: US PROV 60/009,918
; EARLIER FILING DATE: 1996-01-12
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:

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OTHER INFORMATION: oligonucleotide  
US-08-787-321-12

Query Match 0.5%; Score 24.2; DB 3; Length 30;  
Best Local Similarity 89.7%; Pred. No. 6.8e+03;  
Matches 26; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5183 CTCTCACACAAAAA 5211  
Db 1 CACACAAAAA 29

## RESULT 10

US-08-566-037A-22/c  
Sequence 22, Application US/08566037A  
Patent No. 5756295  
GENERAL INFORMATION:

APPLICANT: Haruo ONDA et al.  
TITLE OF INVENTION: DNA PRIMER AND A METHOD FOR  
SCREENING DNAs  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack  
STREET: 805 Fifteenth Street, N.W., #700  
CITY: Washington  
STATE: D.C.  
COUNTRY: U.S.A.  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/566,037A

Filing Date: December 1, 1995

CLASSIFICATION: 435

Prior Application Data:

APPLICATION NUMBER:

Filing Date:

ATTORNEY/AGENT INFORMATION:

NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-8850

TELEFAX:

TELEX:

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 24

TYPE: Nucleic acid

STRANDEDNESS: Double

TOPOLOGY: Linear

MOLECULE TYPE: Other nucleic acid

US-08-566-037A-22

Query Match 0.5%; Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 6.7e+03;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5212 CCATGGTACCGGATCTCGAATT 5235

Db 24 CCATGGTACCGGATCTCGAATT 1

## RESULT 11

US-10-003-998A-7

Sequence 7, Application US/10003998A

Patent No. 6664064

GENERAL INFORMATION:

APPLICANT: Roche Diagnostics GmbH

TITLE OF INVENTION: Method for melting curve analysis of repetitive PCR  
products

FILE REFERENCE: 5438/00/EP

CURRENT APPLICATION NUMBER: US/10/003,998A

CURRENT FILING DATE: 2001-11-14

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 7

LENGTH: 29

TYPE: DNA

ORGANISM: Homo sapiens

US-10-003-998A-7

Query Match 0.5%; Score 23.8; DB 4; Length 29;  
Best Local Similarity 92.6%; Pred. No. 8.4e+03;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5188 AACAAAAA 5214

Db 3 AAAAAA 29

## RESULT 12

US-08-621-914A-3/c

Sequence 3, Application US/08621914A

Patent No. 5707807

GENERAL INFORMATION:

APPLICANT: KATO, KIKUYA

TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESSEE: FENNIE & EDMONDS

STREET: 1155 AVENUE OF THE AMERICAS

CITY: NEW YORK

STATE: NY

COUNTRY: USA

ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,914A

Filing Date: 26-MAR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: LAWRENCE III, STANTON T.

REGISTRATION NUMBER: 25,736

REFERENCE/DOCKET NUMBER: 7005-107-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: other nucleic acid

US-08-621-914A-3

Query Match 0.4%; Score 23.4; DB 1; Length 26;  
Best Local Similarity 96.0%; Pred. No. 9.9e+03;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5187 CAACAAAAA 5211

Db 26 CAAAAA 2

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RESULT 13
US-09-648-040-4
; Sequence 4, Application US/09648040
; Patent No. 6436665
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kuimelis
; TITLE OF INVENTION: METHODS FOR CODING AND SORTING IN VITRO
; FILE REFERENCE: TRANSLATED PROTEINS
; CURRENT APPLICATION NUMBER: US/09/648,040
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,261
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO. 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: n at position 10 can be a, t, c, or g.
US-09-648-040-4

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Query Match 0.4%; Score 23.4; DB 4; Length 30;
Best Local Similarity 92.3%; Pred. No. 1.1e+04;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5188 AACAAAAA...AAAAAAC 5213
Db 5 AAAAAA...AAAAAAC 30

```

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RESULT 14
US-08-621-914A-1/c
; Sequence 1, Application US/08621914A
; Patent No. 5707807
; GENERAL INFORMATION:
; APPLICANT: KATO, KIKUYA
; TITLE OF INVENTION: MOLECULAR INDEXING FOR EXPRESSED GENE
; FILE REFERENCE: ANALYSIS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,914A
; FILING DATE: 26-MAR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LAWRENCE III, STANTON T.
; REGISTRATION NUMBER: 25,736
; REFERENCE/DOCKET NUMBER: 7005-107-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown

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; TOPOLOGY: unknown
; MOLECULE TYPE: other nucleic acid
US-08-621-914A-1
Query Match 0.4%; Score 22.8; DB 1; Length 26;
Best Local Similarity 92.3%; Pred. No. 1.4e+04;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5186 TCACAAAAA...AAAAAAA 5211
Db 26 TAAAAA...AAAAAAA 1

RESULT 15
US-09-522-217-38/c
; Sequence 38, Application US/09522217
; Patent No. 6307024
; GENERAL INFORMATION:
; APPLICANT: No. 6307024ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAIL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/522,217
; CURRENT FILING DATE: 2000-03-09
; EARLIER APPLICATION NUMBER: US 60/123,547
; EARLIER FILING DATE: 1999-03-09
; EARLIER APPLICATION NUMBER: US 60/123,904
; EARLIER FILING DATE: 1999-03-11
; EARLIER APPLICATION NUMBER: US 60/142,013
; EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-09-522-217-38

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Query Match 0.4%; Score 22.8; DB 4; Length 26;
Best Local Similarity 92.3%; Pred. No. 1.4e+04;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5186 TCACAAAAA...AAAAAAA 5211
Db 26 TAAAAA...AAAAAAA 1

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Job time : 325 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 15, 2004, 16:24:03 ; Search time 2188 Seconds  
(without alignments)  
12040.701 Million cell updates/sec

Title: US-10-019-595-1  
Perfect score: 5236  
Sequence: 1 cgagcgcgccgttgagc.....gtaccggatctctgaattc 5236

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3304383 seqs, 2515761380 residues  
Total number of hits satisfying chosen parameters: 1414684

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:  
6: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:  
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10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:  
13: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:  
14: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:  
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17: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:  
18: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:  
19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24.4	0.5	29	9	US-09-282-734-3
2	24.4	0.5	29	10	US-09-876-235-8
3	24.4	0.5	29	15	US-10-348-627-3
4	24.4	0.5	29	17	US-10-057-783A-41
5	23.4	0.4	26	9	US-09-099-823-14
6	23.4	0.4	30	15	US-10-217-914-4
7	22.8	0.4	26	9	US-09-922-480-7
8	22.8	0.4	26	9	US-09-923-236-7
9	22.8	0.4	26	9	US-09-923-246-38
10	22.8	0.4	26	9	US-09-922-469-7
11	22.8	0.4	26	15	US-10-295-723-38
12	22.8	0.4	26	17	US-10-659-684-38
13	22.6	0.4	26	9	US-09-922-480-6
14	22.6	0.4	26	9	US-09-923-236-6

c 15 22.6 0.4 26 9 US-09-922-469-6 Sequence 6, Appli  
c 16 22.6 0.4 26 15 US-10-039-876A-10 Sequence 10, Appli  
c 17 22.6 0.4 26 15 US-10-196-703-43 Sequence 43, Appli  
c 18 22.6 0.4 26 15 US-10-352-263A-36 Sequence 36, Appli  
c 19 22.6 0.4 26 16 US-10-224-289-20 Sequence 20, Appli  
c 20 22.6 0.4 27 13 US-10-071-214-42 Sequence 42, Appli  
c 21 22.6 0.4 27 13 US-09-920-342-12 Sequence 12, Appli  
c 22 22.4 0.4 24 9 US-09-920-313-148 Sequence 148, App  
c 23 22.4 0.4 24 10 US-09-949-308B-6 Sequence 6, Appli  
c 24 22.4 0.4 24 10 US-09-888-326-841 Sequence 841, App  
c 25 22.4 0.4 24 10 US-09-776-479-433 Sequence 433, App  
c 26 22.4 0.4 24 10 US-09-776-479-961 Sequence 961, App  
c 27 22.4 0.4 24 10 US-09-776-479-962 Sequence 962, App  
c 28 22.4 0.4 24 13 US-10-058-270A-140 Sequence 140, App  
c 29 22.4 0.4 24 13 US-10-314-578-433 Sequence 433, App  
c 30 22.4 0.4 24 13 US-10-314-578-961 Sequence 961, App  
c 31 22.4 0.4 24 13 US-09-776-479-433 Sequence 433, App  
c 32 22.4 0.4 24 13 US-09-776-479-961 Sequence 961, App  
c 33 22.4 0.4 24 13 US-09-776-479-962 Sequence 962, App  
c 34 22.4 0.4 24 13 US-10-671-628-10 Sequence 10, Appli  
c 35 22.4 0.4 24 14 US-10-043-415-4 Sequence 4, Appli  
c 36 22.4 0.4 24 15 US-10-112-653-415 Sequence 415, App  
c 37 22.4 0.4 24 15 US-10-112-653-919 Sequence 919, App  
c 38 22.4 0.4 24 15 US-10-112-653-920 Sequence 920, App  
c 39 22.4 0.4 24 15 US-10-017-995-433 Sequence 433, App  
c 40 22.4 0.4 24 15 US-10-017-995-961 Sequence 961, App  
c 41 22.4 0.4 24 15 US-10-017-995-962 Sequence 962, App  
c 42 22.4 0.4 24 15 US-10-058-513-39 Sequence 39, Appli  
c 43 22.4 0.4 24 15 US-10-272-502A-2 Sequence 2, Appli  
c 44 22.4 0.4 24 15 US-10-224-523-53 Sequence 53, Appli  
c 45 22.4 0.4 24 15 US-10-224-523-53 Sequence 53, Appli

ALIGNMENTS

RESULT 1  
US-09-282-734-3  
; Sequence 3, Application US/09282734A  
; Publication No. US20020182597A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert G. Kuimelis et al.  
; TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS  
; FILE REFERENCE: 50036/009002  
; CURRENT APPLICATION NUMBER: US/09/282,734A  
; CURRENT FILING DATE: 1999-03-03  
; EARLIER APPLICATION NUMBER: 60/080,686  
; EARLIER FILING DATE: 1998-04-03  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 3  
; LENGTH: 29  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide used for attaching puromycin  
US-09-282-734-3

Query Match 0.5%; Score 24.4; DB 9; Length 29;  
Best Local Similarity 96.2%; Pred. No. 2.7e+04;  
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5188 AACAAAAA...AAAAAACCC 5213  
Db 4 AAAAAA...AAAAAACCC 29

RESULT 2  
US-09-876-235-8  
; Sequence 8, Application US/09876235  
; Publication No. US2003002236A1  
; GENERAL INFORMATION:  
; APPLICANT: Szostak, Jack W.

; APPLICANT: Roberts, Richard W.  
 ; APPLICANT: Liu, Rihe  
 ; TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN  
 ; FILE REFERENCE: FUSIONS  
 ; CURRENT APPLICATION NUMBER: US/09/876,235  
 ; CURRENT FILING DATE: 2001-06-06  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,190  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/035,963  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-01-21  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/064,491  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-06  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/007,005  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-14  
 ; NUMBER OF SEQ ID NOS: 38  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 8  
 ; LENGTH: 29  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Translation template  
 US-09-876-235-8

Query Match 0.5%; Score 24.4; DB 10; Length 29;  
 Best Local Similarity 96.2%; Pred. No. 2.7e-04;  
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 5188 AACAAAAA...AAAAAACC 5213  
 Db 4 AAAAAA...AAAAAACC 29

RESULT 3  
 US-10-348-627-3  
 ; Sequence 3, Application US/10348627  
 ; Publication No. US20030143616A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robert G. Kuimelis et al.  
 ; TITLE OF INVENTION: ADDRESSABLE PROTEIN ARRAYS  
 ; FILE REFERENCE: 50036/009002  
 ; CURRENT APPLICATION NUMBER: US/10/348,627  
 ; CURRENT FILING DATE: 2003-01-22  
 ; PRIOR APPLICATION NUMBER: US/09/282,734A  
 ; PRIOR FILING DATE: 1999-03-03  
 ; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/080,686  
 ; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-03  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 29  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Oligonucleotide used for attaching puromycin  
 US-10-348-627-3

Query Match 0.5%; Score 24.4; DB 15; Length 29;  
 Best Local Similarity 96.2%; Pred. No. 2.7e-04;  
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 5188 AACAAAAA...AAAAAACC 5213  
 Db 4 AAAAAA...AAAAAACC 29

RESULT 4  
 US-10-057-783A-41  
 ; Sequence 41, Application US/10057783A  
 ; Publication No. US20040091955A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Forster, Anthony C.

; TITLE OF INVENTION: Process and compositions for peptide, protein and  
 ; FILE REFERENCE: peptidomimetic synthesis  
 ; CURRENT APPLICATION NUMBER: US/10/057,783A  
 ; CURRENT FILING DATE: 2002-01-25  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: Patentin Ver. 2.1  
 ; SEQ ID NO 41  
 ; LENGTH: 29  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: FROM SYNTHETIC  
 ; OTHER INFORMATION: DNA  
 US-10-057-783A-41

Query Match 0.5%; Score 24.4; DB 17; Length 29;  
 Best Local Similarity 96.2%; Pred. No. 2.7e-04;  
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 5188 AACAAAAA...AAAAAACC 5213  
 Db 4 AAAAAA...AAAAAACC 29

RESULT 5  
 US-09-099-823-14/c  
 ; Sequence 14, Application US/09099823  
 ; Patent No. US20020018990A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BILLING-MEDEL, PATRICIA  
 ; APPLICANT: COHEN MAURICE  
 ; APPLICANT: COLPITTS, TRACEY L.  
 ; APPLICANT: FRIEDMAN, PAULA N.  
 ; APPLICANT: GORDON, JULIAN  
 ; APPLICANT: GRANADOS, EDWARD N.  
 ; APPLICANT: HODGES, STEVEN C.  
 ; APPLICANT: KLASS, MICHAEL R.  
 ; APPLICANT: KRATOCHVIL, JON D.  
 ; APPLICANT: RUSSELL, JOHN C.  
 ; APPLICANT: SCHEFFEL, CHRISTI  
 ; APPLICANT: STROUPE, STEPHEN D.  
 ; APPLICANT: YU, HONG  
 ; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
 ; FOR DETECTING DISEASES OF THE BREAST  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Abbott Laboratories  
 ; STREET: 100 Abbott Park Road  
 ; CITY: Abbott Park  
 ; STATE: IL  
 ; COUNTRY: USA  
 ; ZIP: 60064-3500  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/099,823  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/879,354  
 ; FILING DATE: 20-JUN-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Becker, Cheryl L.  
 ; REGISTRATION NUMBER: 35,441  
 ; REFERENCE/DOCKET NUMBER: 6120.US.PI  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 847/935-1729  
 ; TELEFAX: 847/938-2623  
 ; TELEX:

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; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 26 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
US-09-099-823-14
Query Match          0.4%; Score 23.4; DB 9; Length 26;
Best Local Similarity 96.0%; Pred. No. 4.7e+04;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5187 CAACAAAAA 5211
Db 26 CAACAAAAA 2

RESULT 6
US-10-217-914-4
; Sequence 4, Application US/10217914
; Publication No. US20030013160A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Kumelis
; TITLE OF INVENTION: METHODS FOR CODING AND SORTING IN VITRO
; FILE REFERENCE: 50036/032002
; CURRENT APPLICATION NUMBER: US/10/217,914
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 09/548,040
; PRIOR FILING DATE: 2000-08-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Encoding molecule
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: n at position 10 can be a, t, c, or g.
US-10-217-914-4

Query Match          0.4%; Score 23.4; DB 15; Length 30;
Best Local Similarity 92.3%; Pred. No. 5.3e+04;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5188 AACAAAAA 5213
Db 5 AACAAAAA 30

RESULT 7
US-09-922-480-7/c
; Sequence 7, Application US/09922480
; Patent No. US20020081701A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,480
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

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; OTHER INFORMATION: Oligonucleotide primer ZC77644
US-09-922-480-7

Query Match          0.4%; Score 22.8; DB 9; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.8e+04;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5186 TCAACAAAAA 5211
Db 26 TAAACAAAAA 1

RESULT 8
US-09-923-236-7/c
; Sequence 7, Application US/09923236
; Patent No. US20020090677A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/923,236
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC77644
US-09-923-236-7

Query Match          0.4%; Score 22.8; DB 9; Length 26;
Best Local Similarity 92.3%; Pred. No. 6.8e+04;
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5186 TCAACAAAAA 5211
Db 26 TAAACAAAAA 1

RESULT 9
US-09-923-246-38/c
; Sequence 38, Application US/09923246
; Patent No. US2002012846A1
; GENERAL INFORMATION:
; APPLICANT: No. US2002012846A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAIL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 2000-03-09
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1999-03-11
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 26

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-09-923-246-38

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  Best Local Similarity 92.3%; Pred. No. 6.8e+04;
  Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5186 TCAACAAAAA 5211
Db 26 TAAAAA 1

RESULT 10
US-09-922-469-7/c
; Sequence 7, Application US/09922469
; Patent No. US20020173027A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,469
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-09-922-469-7

  Query Match      0.4%  Score 22.8; DB 9; Length 26;
  Best Local Similarity 92.3%; Pred. No. 6.8e+04;
  Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5186 TCAACAAAAA 5211
Db 26 TAAAAA 1

RESULT 11
US-10-295-723-38/c
; Sequence 38, Application US/10295723
; Publication No. US20030125524A1
; GENERAL INFORMATION:
; APPLICANT: Novak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/10/295,723
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 09/522,217
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/123,547
; PRIOR FILING DATE: 1999-03-09
; PRIOR APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7764a
US-10-295-723-38

  Query Match      0.4%  Score 22.8; DB 17; Length 26;
  Best Local Similarity 92.3%; Pred. No. 6.8e+04;
  Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5186 TCAACAAAAA 5211
Db 26 TAAAAA 1

RESULT 13
US-09-922-480-6/c
; Sequence 6, Application US/09922480
; Patent No. US20020081701A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Adler, David A.
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; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; FILE REFERENCE: 97-71
; CURRENT APPLICATION NUMBER: US/09/922,480
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7231
US-09-922-480-6

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Query Match          0.4%; Score 22.6; DB 9; Length 26;
Best Local Similarity 92.0%; Pred. No. 7.7e+04;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 5187 CAACAAACAAAAA 5211
Db 26 BAAAAA 2

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RESULT 14

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US-09-923-236-6/c
; Sequence 6, Application US/09923236
; Patent No. US20020090677A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; CURRENT APPLICATION NUMBER: US/09/923,236
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7231
US-09-923-236-6

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Query Match          0.4%; Score 22.6; DB 9; Length 26;
Best Local Similarity 92.0%; Pred. No. 7.7e+04;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 5187 CAACAAACAAAAA 5211
Db 26 BAAAAA 2

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RESULT 15

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US-09-922-469-6/c
; Sequence 6, Application US/09922469
; Patent No. US20020173027A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SECRETED SALIVARY ZSIG63 POLYPEPTIDE
; CURRENT APPLICATION NUMBER: US/09/922,469
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/124,820
; PRIOR FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6

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; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer ZC7231
US-09-922-469-6
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Best Local Similarity 92.0%; Pred. No. 7.7e+04;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 5187 CAACAAACAAAAA 5211
Db 26 BAAAAA 2

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Search completed: September 16, 2004, 02:22:36  
Job time : 2189 secs

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Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0303 row: 1 column: 24  
 Seq primer: CGTTGTAACAGCAGCCGAGT  
 Class: plasmid ends  
 High quality sequence stop: 28.

## FEATURES

source

1. .28  
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 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0303L24"  
 /sex="male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /notes="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pWD42 (G14732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Query Match 0.5%; Score 24.4; DB 28; Length 28;  
 Best Local Similarity 96.2%; Pred. No. 1.6e+07;  
 Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5187 CAACAAAAA.....AAAAAAC 5212

Db 28 CAAAAA.....AAAAAAC 3

## RESULT 2

T67079

LOCUS

DEFINITION  
 ya52f07.r3 Soares fetal liver spleen INFIS Homo sapiens CDNA clone  
 IMAGE:66565 5' similar to gb:X02492 INTERFERON-INDUCED PROTEIN 6-16  
 PRECURSOR (HUMAN); mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 29)  
 Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
 Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,  
 Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,  
 Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and  
 Wilson, R.

TITLE

JOURNAL

COMMENT

The WashU-Merck EST Project  
 Unpublished (1995)  
 Contact: Wilson RK  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu

High quality sequence starts: 1  
 High quality sequence stops: 1  
 Source: IMAGE Consortium, LLNL  
 This clone is available royalty-free through LLNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Trace considered overall poor quality  
 Seq primer: T7

High quality sequence stop: 1.

## FEATURES

source

1. .29  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:66565"  
 /sex="male"

/dev\_host="20 week-post conception fetus"  
 /lab\_host="DH10B (ampicillin resistant)"  
 /clone\_lib="Soares fetal liver spleen INFIS"  
 /note="Organ: liver and spleen; Vector: p77T3D (Pharmacia)  
 with a modified polylinker; Site\_1: Pac I; Site\_2: Eco RI;  
 1st strand cDNA was primed with a Pac I - oligo(dT) primer  
 [5' AACGCGAAGATTAATAAGATCTTTTCTTTTCTTTT 3'],  
 double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Pac I and cloned into the Pac I  
 and Eco RI sites of the modified p77T3 vector. Library  
 went through one round of normalization. Library  
 constructed by Bento Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 0.5%; Score 24.4; DB 14; Length 29;

Best Local Similarity 92.6%; Pred. No. 1.6e+07;

Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5184 TCTCAACAAAAA.....AAAAAAA 5210

Db 3 TCTCAAAAAA.....AAAAAAA 29

## RESULT 3

AZ819924

LOCUS

DEFINITION

29 bp DNA linear GSS 20-FEB-2001  
 clone UUGC2M0091A19 R, genomic survey sequence.

ACCESSION

AZ819924

VERSION

AZ819924.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 29)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islan, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von  
 Niederhauser, A. and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0091 row: A column: 19  
 Seq primer: CACACAGAAACAGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 29.  
 Location/Qualifiers  
 1. .29



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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0091A19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

ORIGIN

Query Match	0.5%;	Score 24.4;	DB 28;	Length 29;
Best Local Similarity	96.2%;	Pred. No. 1.6e+07;		
Matches	25;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;

QY 5188 AACAAAAA...AAAAAAC 5213

DB 3 AAAAAAAAAAAAAAAAAAAC 28

RESULT 4

AZ458127/c

LOCUS

DEFINITION

1M0261124R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0261124 R, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Robert B. Weiss

UNIVERSITY OF UTAH

RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

TEL: 801 585 5606

FAX: 801 585 7177

EMAIL: dunn@genetics.utah.edu

INSERT LENGTH: 10000

STD ERROR: 0.00

PLATE: 0261

ROW: 1

COLUMN: 24

SEQ PRIMER: CACACAGAAACAGCTATGACC

CLASS: plasmid ends

HIGH QUALITY SEQUENCE STOP: 30.

FEATURES

Location/Qualifiers

1..30

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/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0091A19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
```

ORIGIN

Query Match	0.5%;	Score 24.4;	DB 28;	Length 29;
Best Local Similarity	96.2%;	Pred. No. 1.6e+07;		
Matches	25;	Conservative	0;	Mismatches 1; Indels 0; Gaps 0;

QY 5188 AACAAAAA...AAAAAAC 5213

DB 3 AAAAAAAAAAAAAAAAAAAC 28

RESULT 5

AZ809971/c

LOCUS

DEFINITION

2M0074C14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0074C14 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT: Robert B. Weiss

UNIVERSITY OF UTAH

RM. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

TEL: 801 585 5606

FAX: 801 585 7177

EMAIL: dunn@genetics.utah.edu

INSERT LENGTH: 10000

STD ERROR: 0.00

PLATE: 0074

ROW: C

COLUMN: 14

SEQ PRIMER: CGTTGTAACGACGCCAGT

CLASS: plasmid ends

HIGH QUALITY SEQUENCE STOP: 28.

FEATURES

Location/Qualifiers

1..28



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Query Match      0.4%; Score 23.4; DB 14; Length 25;
Best Local Similarity 96.0%; Pred. No. 2.4e+07;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5188 AACAAAAA...AAAAAAAAAAC 5212
Db 25 AAAAAAAAAA...AAAAAAAAAAC 1

RESULT 8
CF296851/c      26 bp mRNA linear EST 14-AUG-2003
LOCUS 30DGS--07-G13.b1 Rice leaf plasmid cDNA library I (30DGS) Oryza
DEFINITION sative cDNA clone 30DGS--07-G13, mRNA sequence.
ACCESSION CF296851
VERSION CF296851.1 GI:33665984
KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 26)
AUTHORS Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
TITLE Large-scale Sequencing Analysis of Rice ESTs
JOURNAL Unpublished (2003)
COMMENT Contact: Nahm B.H.
Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
of Bioscience and Bioinformatics, Myongji University
Yongin, Gyeonggi, Korea
Tel: 82 31 330 6193
Fax: 82 31 321 6355
Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES
source
1..26
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="Nackdong"
/db_xref="taxon:4530"
/clone="30DGS--07-G13"
/tissue_type="leaf"
/dev_stage="30 days after germination"
/lab_host="E.coli DH10B"
/clone_lib="Rice leaf plasmid cDNA library I (30DGS)"
/notes="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
with oligoribonucleotides and then used as templates for
RT-PCR."

ORIGIN
Query Match      0.4%; Score 23.4; DB 14; Length 26;
Best Local Similarity 96.0%; Pred. No. 2.4e+07;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5188 AACAAAAA...AAAAAAAAAAC 5212
Db 25 AAAAAAAAAA...AAAAAAAAAAC 1

RESULT 9
AZ485624      26 bp DNA linear GSS 05-OCT-2000
LOCUS 1W0313H11F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
DEFINITION clone UUC1W0313H11 F, genomic survey sequence.
ACCESSION AZ485624
VERSION AZ485624.1 GI:10651606
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Query Match      0.4%; Score 23.4; DB 28; Length 26;
Best Local Similarity 96.0%; Pred. No. 2.4e+07;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5191 AAAAAAAAAA...AAAAAACCAT 5215
Db 1 AAAAAAAAAA...AAAAAATCCAT 25

RESULT 10
N52529/c      27 bp mRNA linear EST 15-FEB-1996
LOCUS YV35a12.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
DEFINITION IMAGE:244702 3, similar to gb:X68242 PUTATIVE HIV-1 INDUCED PROTEIN
HIN-1 (HUMAN);, mRNA sequence.
ACCESSION N52529
VERSION N52529.1 GI:1193695
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 27)
REFERENCE

```

```

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Rilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D. Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0313 row: H column: 11
Seq primer: CGTTGTAAACGACGCCAGT
Class: plasmid ends
High quality sequence stop: 26.

FEATURES
Location/Qualifiers
1..26
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0313H11"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-."
/clone_lib="Mouse 10kb plasmid UGCGIM library"
/notes="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 [gi|4732114|gb|AF129072.1|, a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN
Query Match      0.4%; Score 23.4; DB 28; Length 26;
Best Local Similarity 96.0%; Pred. No. 2.4e+07;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5191 AAAAAAAAAA...AAAAAACCAT 5215
Db 1 AAAAAAAAAA...AAAAAATCCAT 25

RESULT 10
N52529/c      27 bp mRNA linear EST 15-FEB-1996
LOCUS YV35a12.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone
DEFINITION IMAGE:244702 3, similar to gb:X68242 PUTATIVE HIV-1 INDUCED PROTEIN
HIN-1 (HUMAN);, mRNA sequence.
ACCESSION N52529
VERSION N52529.1 GI:1193695
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 27)
REFERENCE

```

## AUTHORS

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and Wilson, R.

TITLE  
JOURNAL  
COMMENT

The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information.  
Trace considered overall poor quality  
Seq primer: ml3 -40 forward  
High quality sequence stop: 1.

## FEATURES

source  
1. .27  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:3793948"  
/db\_xref="taxon:9606"  
/clone="IMAGE:244702"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="PH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal liver spleen INFLS"  
/notes="Organ: liver and spleen; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5'-AAGCTCGAAGATTAATAAGATCTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

## ORIGIN

Query Match 0.4%; Score 23.4; DB 14; Length 27;  
Best Local Similarity 92.3%; Pred. No. 2.3e+07;  
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5186 TCACCAAAAAAAAAAAAAAAAAAAAA 5211  
|||  
Db 26 TCNAAAAAAAAAAAAAAAAAAAAA 1

## RESULT 11

AL587582/c  
LOCUS 28 bp mRNA linear EST 02-MAR-2001  
DEFINITION AL587582 BP Chicken Brain Library Gallus gallus cDNA clone  
ROS059D03, mRNA sequence.

ACCESSION AL587582.1 GI:13192616  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Gallus gallus (chicken)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
1 (bases 1 to 28)

## REFERENCE

Murray, F.  
BP Chicken Brain Library  
Unpublished (2001)  
Contact: Frazer Murray  
Dept. Genomics and Bioinformatics  
Roslin Institute  
Roslin, Midlothian, EH25 9PS, UK  
Tel: +44 (0)131 527 4200  
Fax: +44 (0)131 440 0434  
Email: frazer.murray@bbsrc.ac.uk

CGCGCGCTTTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clontech (\*6854-  
Seq primer: ML3F.

## FEATURES

source  
1. .28  
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/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/clone="ROS059D03"  
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/dev\_stage="Unknown"  
/lab\_host="DH10B"  
/clone\_lib="BP Chicken Brain Library"  
/notes="Vector: ESORT1; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. 5' adaptor sequence: 5' TCGACCTCGAG 3'; 3' adaptor sequence: 5' CGCGCGCTTTTTTTTTTTTTTTT 3' Poly A RNA purchased from Clontech (\*6854-1)"

## ORIGIN

Query Match 0.4%; Score 23.4; DB 9; Length 28;  
Best Local Similarity 92.3%; Pred. No. 2.3e+07;  
Matches 24; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5190 CAAAAAATAAAAAAAAAAAAAAACCAT 5215  
|||||  
Db 26 CAAAAAATAAAAAAAAAAAAAAANAAT 1

## RESULT 12

CF299294  
LOCUS 28 bp mRNA linear EST 15-AUG-2003  
DEFINITION 7LEAF-03-E04.g1 Rice leaf plasmid cDNA library II (7LEAF) Oryza sativa cDNA clone 7LEAF--03-E04, mRNA sequence.

ACCESSION CF299294  
VERSION  
KEYWORDS  
SOURCE  
EST.  
Oryza sativa

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

1 (bases 1 to 28)  
Kim, J.S., Jun, X.M., Cheong, P.J., Kim, M.J., Lee, T.H., Shin, Y.C., Song, S.I., Kim, J.K., Kim, Y.-K. and Nahm, B.H.  
Large-scale Sequencing Analysis of Rice ESTs  
Unpublished (2003)  
Contact: Nahm B.H.

Genomics and Genetics Institute, GreenGene Biotech Inc.; Division of Bioscience and Bioinformatics, Myongji University  
Yongin, Gyeonggi, Korea  
Tel: 82 31 330 6193  
Fax: 82 31 321 6355  
Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

## FEATURES

source  
1. .28  
Location/Qualifiers  
/organism="Oryza sativa"  
/mol\_type="mRNA"  
/cultivar="Nackdong"  
/db\_xref="taxon:4530"  
/clone="7LEAF--03-E04"  
/tissue\_type="leaf"  
/dev\_stage="7 days after germination"  
/lab\_host="E.coli DH10B"  
/clone\_lib="Rice leaf plasmid cDNA library II (7LEAF)"  
/notes="Vector: pCR4-TOPO; Site 1: EcoRI; mRNA was capped with oligoribonucleotides and then used as templates for RT-PCR."

## ORIGIN

Query Match 0.4%; Score 23.4; DB 14; Length 28;  
Best Local Similarity 96.0%; Pred. No. 2.3e+07;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



Email: bhnahm@bio.com, bhnahm@bio.myongji.ac.kr.

# FEATURES

source

Location/Qualifiers

1..24

/organism="Oryza sativa"

/mol\_type="mRNA"

/cultivar="Nackdong"

/db\_xref="taxon:4510"

/clone="ABF-07-P12"

/tissue\_type="leaf"

/dev\_stage="14 days after germination"

/lab\_host="E.coli DH10B"

/clone\_lib="ABF3-overexpressing transgenic rice plasmid

CDNA library (ABF)"

/note="Vector: PCR4-TOPO; Site 1: EcoRI; Leaf was dried for 2hrs. Oligo-capped mRNA was reverse transcribed and then used for PCR. mRNA was prepared from ABA-responsive element binding transcription factor 3 overexpression line."

## ORIGIN

Query Match 0.4%; Score 23; DB 14; Length 24;

Best Local Similarity 100.0%; Pred. No. 2.8e+07; Indels 0; Gaps 0;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

• QY 5191 AAAAAAAAAAAAAAAAAAAACC 5213

Db 23 AAAAAAAAAAAAAAAAAAAACC 1

• Search completed: September 16, 2004, 01:40:37

Job time : 12085 secs